SEQUENCE LISTING

<110> McKeon, F.
      Kayako, K.
      Ryeom, S.

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<140> 09/575,580
<141> 2000-05-22

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    Cys  Glu  Ser  Asp  Gln  Glu  Asn  Glu  Glu  Glu  Glu  Glu  Glu  Met  Glu  Arg
                        165                       170                     175

    Met  Lys  Arg  Pro  Lys  Pro  Lys  Ile  Ile  Gln  Thr  Arg  Arg  Pro  Glu  Tyr
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    Arg  Asp  Trp  Ala  Val  Thr  Gln  Cys  Phe  Ala  Glu  Glu  Ala  Phe  Gln  Ala
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    Leu  Thr  Asp  Phe  Ser  Asp  Leu  Pro  Asn  Ser  Leu  Phe  Ala  Cys  Asn  Val
         50                        55                      60
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His Gln Ser Val Phe Glu Glu Glu Ser Lys Glu Lys Phe Glu Gly
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Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe Lys Ser
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Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala Ala Arg
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Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Pro
            115   120   125

Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu
        130   135   140

His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro
145   150   155   160

Ser Ser Pro Ser Val Gly Trp Lys Pro Ile Ser Asp Ala Thr Pro Val
                165   170   175

Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu
                180   185   190

Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val
        195   200   205

His Val Cys Asp Ser Asp Met Glu Arg Glu Glu Asp Pro Lys Thr Ser
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<213> Homo sapiens

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Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Glu Gly Leu Phe Arg
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Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
            35   40   45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
        50   55   60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65   70   75   80

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Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
                85                  90                  95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
            100                 105                 110

Pro Val Gly Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
        115                 120                 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
    130                 135                 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145                 150                 155                 160

Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
                165                 170                 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
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<213> Homo sapiens

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Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn Phe
            20                  25                  30

Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys Thr
            35                  40                  45

Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu His
    50                  55                  60

Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu
65                  70                  75                  80

Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp
            85                  90                  95

Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu
            100                 105                 110

Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr Pro
        115                 120                 125

Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu
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Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr
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Arg Arg Pro Glu Tyr Thr Pro Ile His Leu
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<211> 197
<212> PRT
<213> Cricetulus griseus

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Met His Phe Arg Asp Phe Asn Tyr Asn Phe Ser Ser Leu Ile Ala Cys
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Val Ala Asn Gly Asp Val Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
                    20                    25                    30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
                35                    40                    45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
        50                    55                    60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65                    70                    75                    80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
                85                    90                    95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
                100                   105                   110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
                115                   120                   125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
                130                   135                   140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145                   150                   155                   160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Met Glu Arg Met
                165                   170                   175

Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
                180                   185                   190

Pro Ile His Leu Ser
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<212> PRT
<213> Caenorhabditis elegans

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            20              25              30

Ile Val Thr Gln Val Pro Glu Asp Val Phe Asp Asn Lys Gln Asp Lys
            35              40              45

Ala Asn Phe Ser Ser Leu Phe Thr Gln Ile Glu Lys Asp Ile His Phe
        50              55              60

Asp Phe Leu Arg Ser Phe Arg Arg Val Arg Val Ile Phe Ser Ser Pro
65              70              75              80

Glu Asn Ala Thr Ala Ala Lys Leu Ile Val Gln Gly Phe Ser Phe Lys
            85              90              95

Gly His Glu Leu Lys Ala Phe Phe Ala Gln Arg Ile Tyr Met Ser Ala
            100             105             110

Asn Ser Gln Met Leu Ser Pro Pro Pro Leu Glu Lys Gln Phe Leu Ile
        115             120             125

Ser Pro Pro Cys Ser Pro Pro Val Gly Trp Glu Gln Thr Lys Asp Met
    130             135             140

Pro Pro Val Val Cys Asn Phe Asp Leu Met Ala Arg Leu Ala Ser Phe
145             150             155             160

Ala Ile Asp Glu Lys Tyr Glu Val His Asn Gly Asp Glu Leu Thr Pro
            165             170             175

Ala Ile Ile Val His Pro Cys Glu Thr Pro Ile Asp Val Pro Ser Ala
            180             185             190

Ile Glu Met Pro Arg Thr Pro Arg Pro Ser Ser Pro Cys Glu Gln
        195             200             205
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<213> Saccharomyces cerevisiae

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Asp Ile Val Asp Asn Asp Asn Val Glu Arg Ile Gln Val Trp Leu Ser
            20              25              30

Lys Asn Ile Leu Arg Lys Phe Gln Ile Asn Glu Asn Glu Pro Leu Gln
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          35   40   45

Leu Ile Ile Leu Lys Arg Phe Lys Arg Ile Leu Leu Ile Cys Pro Ser
         50   55   60

His Asp Ile Ser Gln His Val Met Asp Ala Ser Arg Ala Leu Glu Met
65   70   75   80

Glu Asn Phe Asn Phe Ser Tyr Ser Leu Gln Asp Gly Gln Arg Asn Leu
                85   90   95

Thr Lys Gln Tyr Leu Lys Val Pro Glu Ser Glu Lys Met Phe Leu Ile
            100   105   110

Ser Pro Pro Ala Ser Pro Pro Pro Glu Phe Asp Phe Ser Lys Cys Glu
        115   120   125

Asp Ala Pro Gln Arg His Ile Gln Ser His Ile Gln Gln Asp Gln Gln
    130   135   140

Gln Arg Leu Glu Ala Ser Gln Leu Leu Pro Asn Asn Pro Asp Lys Asn
145   150   155   160

Asn Asn Gly Thr Phe Thr Leu Leu Lys Ser Lys Val Gly Ala Ile Thr
            165   170   175

Ile Asp Arg Cys Pro Thr Asn Asp Gly Asn Gly Gln Met Gln Leu Ala
        180   185   190

Asp His Val Lys Thr Ala Phe Pro Pro Lys Ser Ile Phe Asp Thr Asp
    195   200   205

Asp Asp Asp
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Leu Gly Lys Val Leu Ala Ser Tyr Asn Asp Lys Ala Val Glu Glu Asp
        35   40   45

Thr Leu Lys Lys Ser Ser Thr Gly Ser Leu Pro Ser Gly Gln Gln Val
    50   55   60

His Cys Gln Tyr Val Leu Asp Asp Pro Asn His Val Glu Gly Ile Ser
65   70   75   80

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Val Asp Gln Ser Leu Gln Val Pro Lys Phe Glu Lys Asn Trp Leu Ile
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Ser Pro Pro Gly Ser Pro Pro Val Gly Trp Glu Pro Ile Val Glu Glu
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Ser Pro Asn Ser Gln His Leu Ala His Asp Ile Gln Leu Lys Leu Asp
         115             120             125

Glu Leu Gly Asn Ala Leu Leu Asn Asp His Ser Ala Gly Pro Gln Ile
    130             135             140

Val Ile Ser Glu His Asn Asn Thr Lys Glu Thr Ser Pro Ser Arg Gln
145             150             155             160

Phe Glu His


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Glu Asp Gly Leu Glu Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
            35               40               45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Val Gln Glu Gln
        50               55               60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Leu Tyr Asp Asp Gln Val Thr
65               70               75               80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
                85               90               95

Pro Ala Arg Ala Arg Ile Glu Leu His Glu Ser Glu Phe His Gly Arg
            100              105              110

Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Val Ser Gly Glu Ala Arg
        115              120              125

Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Thr Lys Gln Phe Leu Ile
    130              135              140

Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser Glu Asp Ala
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Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser
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<212> DNA
<213> Mus musculus

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<223> n=a, c, g, or t

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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: general
      structure

<220>
<221> SITE
<222> (6)
<223> Xaa=any amino acid residue

<400> 28
Pro Lys Pro Lys Ile Xaa Gln Thr Arg Arg Pro Glu
  1               5                   10


<210> 29
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin
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antagonist

<400> 29
Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu
 1   5   10

<210> 30
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: calcineurin
      antagonist

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 1   5   10

<210> 31
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: EGF-derived
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Cys Met His Ile Glu Ser Leu Asp Ser Tyr Thr Cys
 1   5   10

<210> 32
<211> 12
<212> PRT
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<220>
<223> Description of Artificial Sequence: EGF-derived
      peptide

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Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
 1   5   10

<210> 33
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pH-dependent
      membrane-binding internalizing peptide

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<221> SITE
<222> (1)
<223> Xaa=preferably a unique residue, such as Cys or
       Lys, that facilitates chemical conjugation of the
       internalizing peptide to a targeting protein
       conjugate

<220>
<221> SITE
<222> (2)..(3)
<223> Xaa=residues selected to modulate the affinity of
       the internalizing peptide for different membranes

<400> 33
Xaa Xaa Xaa Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala
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Glu Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
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<210> 34
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide
       substrate

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<210> 35
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (4)..(75)

<220>
<223> Description of Artificial Sequence: synthetic
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    Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro
     1   5   10   15

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Lys Lys Lys Arg Lys Val Ala Gly Phe
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<210> 36
<211> 24
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: synthetic
      construct

<400> 36
Met Gly Gly Cys Arg Gly Asp Met Phe Gly Cys Gly Ala Pro Pro Lys
  1               5                  10                  15

Lys Lys Arg Lys Val Ala Gly Phe
            20



<210> 37
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      construct

<220>
<221> CDS
<222> (4)..(225)

<400> 37
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      1               5                  10                  15

agt cag cct aaa act gct tgt acc aat tgc tat tgt aaa aag tgt tgc    96
Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys
                20                  25                  30

ttt cat tgc caa gtt tgt ttc ata aca aaa gcc ctt ggc atc tcc tat   144
Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr
                35                  40                  45

ggc agg aag aag cgg aga cag cga cga aga cct cct caa ggc agt cag   192
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln
            50                  55                  60

act cat caa gtt tct cta agt aag caa gga ttc                        225
Thr His Gln Val Ser Leu Ser Lys Gln Gly Phe
            65                  70
```

<210> 38
<211> 74
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: synthetic
      construct

<400> 38
Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
 1   5   10   15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
            20   25   30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
        35   40   45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
    50   55   60

His Gln Val Ser Leu Ser Lys Gln Gly Phe
65   70

<210> 39
<211> 912
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      construct

<220>
<221> CDS
<222> (4)..(912)

<400> 39
cat atg acc tct cgc cgc tcc gtg aag tcg ggt ccg cgg gag gtt ccg   48
    Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro
     1   5   10   15

cgc gat gag tac gag gat ctg tac tac acc ccg tct tca ggt atg gcg   96
Arg Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala
                20   25   30

agt ccc gat agt ccg cct gac acc tcc cgc cgt ggc gcc cta cag aca   144
Ser Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr
            35   40   45

cgc tcg cgc cag agg ggc gag gtc cgt ttc gtc cag tac gac gag tcg   192
Arg Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser
        50   55   60

gat tat gcc ctc tac ggg ggc tcg tca tcc gaa gac gac gaa cac ccg   240
Asp Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro

gag gtc ccc cgg acg cgg cgt ccc gtt tcc ggg gcg gtt ttg tcc ggc   288
Glu Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly
80   85   90   95

ccg ggg cct gcg cgg gcg cct ccg cca ccc gct ggg tcc gga ggg gcc   336
Pro Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala
                    100   105   110

gga cgc aca ccc acc acc gcc ccc cgg gcc ccc cga acc cag cgg gtg   384
Gly Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val
              115   120   125

gcg act aag gcc ccc gcg gcc ccg gcg gcg gag acc acc cgc ggc agg   432
Ala Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg
              130   135   140

aaa tcg gcc cag cca gaa tcc gcc gca ctc cca gac gcc ccc gcg tcg   480
Lys Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser
              145   150   155

acg gcg cca acc cga tcc aag aca ccc gcg cag ggg ctg gcc aga aag   528
Thr Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys
160   165   170   175

ctg cac ttt agc acc gcc ccc cca aac ccc gac gcg cca tgg acc ccc   576
Leu His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro
                    180   185   190

cgg gtg gcc ggc ttt aac aag cgc gtc ttc tgc gcc gcg gtc ggg cgc   624
Arg Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg
                    195   200   205

ctg gcg gcc atg cat gcc cgg atg gcg gcg gtc cag ctc tgg gac atg   672
Leu Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met
              210   215   220

tcg cgt ccg cgc aca gac gaa gac ctc aac gaa ctc ctt ggc atc acc   720
Ser Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr
              225   230   235

acc atc cgc gtg acg gtc tgc gag ggc aaa aac ctg ctt cag cgc gcc   768
Thr Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala
240   245   250   255

aac gag ttg gtg aat cca gac gtg gtg cag gac gtc gac gcg gcc acg   816
Asn Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr
              260   265   270

gcg act cga ggg cgt tct gcg gcg tcg cgc ccc acc gag cga cct cga   864
Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg
              275   280   285

gcc cca gcc cgc tcc ggt tct cgc ccc aga cgg ccc gtc gag gaa ttc   912
Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe

<210> 40
<211> 303
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: synthetic
      construct

<400> 40
Met Thr Ser Arg Arg Ser Val Lys Ser Gly Pro Arg Glu Val Pro Arg
 1   5   10   15

Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser
            20   25   30

Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg
            35   40   45

Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp
        50   55   60

Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu
65   70   75   80

Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro
                85   90   95

Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly
            100   105   110

Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val Ala
        115   120   125

Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys
        130   ·135   140

Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr
145   150   155   160

Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu
                165   170   175

His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg
            180   185   190

Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu
            195   200   205

Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser
        210   215   220

Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr
225   230   235   240

Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn

```
                245                    250                    255

Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala
            260                    265                    270

Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala
        275                    280                    285

Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu Glu Phe
    290                    295                    300



<210> 41
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
      construct

<220>
<221> CDS
<222> (4)..(120)

<400> 41
cat atg gac gtc gac gcg gcc acg gcg act cga ggg cgt tct gcg gcg     48
    Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala
      1               5                  10                  15

tcg cgc ccc acc gag cga cct cga gcc cca gcc cgc tcc gct tct cgc     96
Ser Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg
                20                  25                  30

ccc aga cgg ccc gtc gag gaa ttc                                    120
Pro Arg Arg Pro Val Glu Glu Phe
            35



<210> 42
<211> 39
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: synthetic
      construct

<400> 42
Met Asp Val Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser
  1               5                  10                  15

Arg Pro Thr Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro
            20                  25                  30

Arg Arg Pro Val Glu Glu Phe
            35
```

<210> 43
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
aggaggtgga tctgc   15

<210> 44
<211> 6
<212> PRT
<213> Mus musculus

<400> 44
Glu Arg Met Arg Arg Pro
  1   5

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
      sequence

<400> 45
Glu Arg Met Pro Pro Arg Arg Asp
  1   5